

Fig. 1

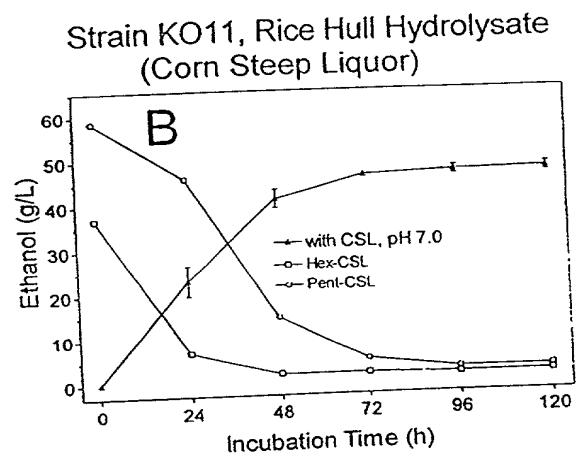
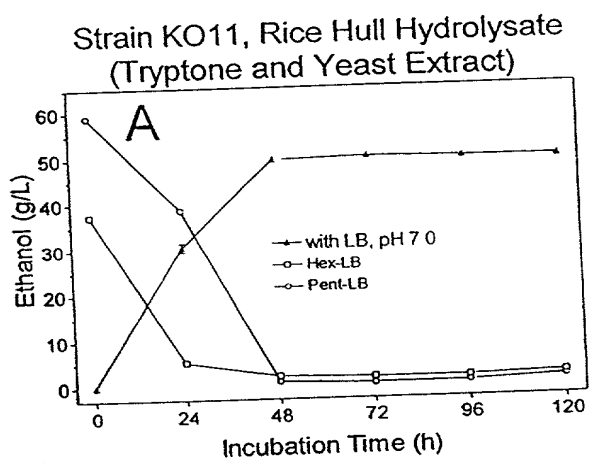


Fig. 2

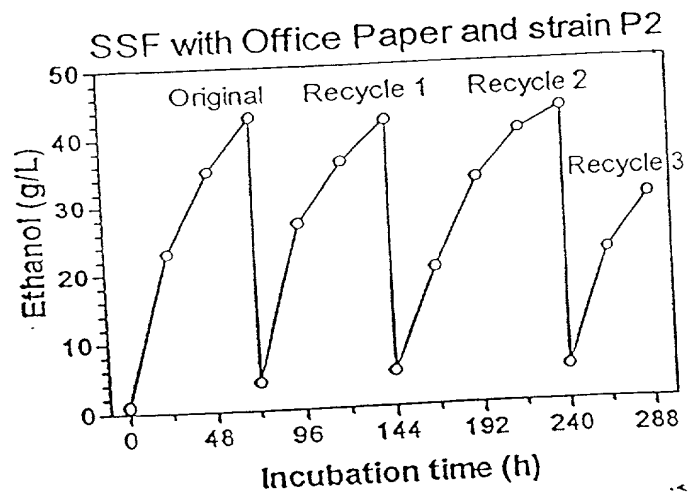


Fig. 3

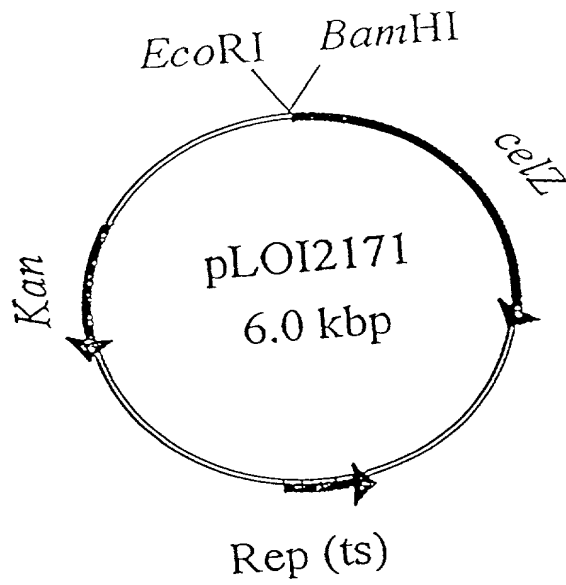


Fig. 4

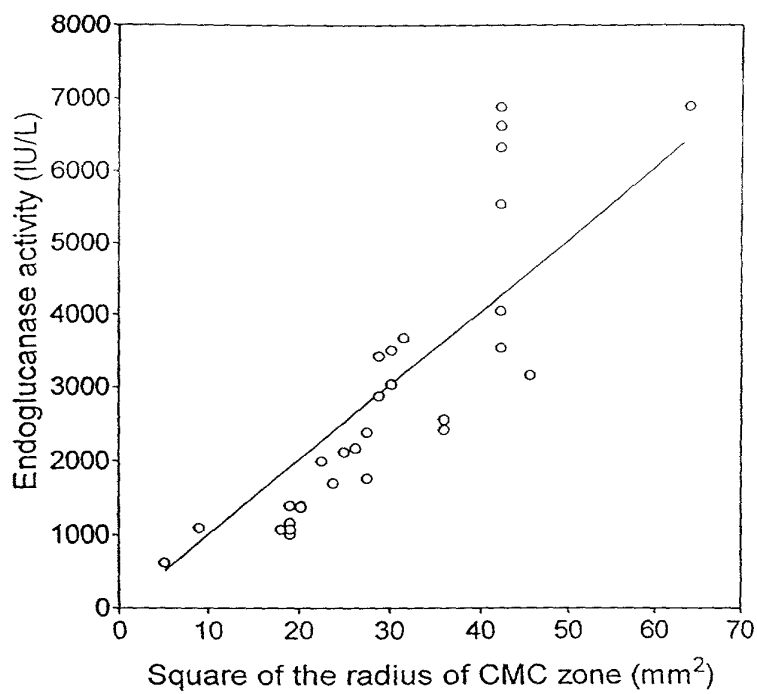


Fig. 5

	-35 region		-10 region	#
1051	CTTTTTTCGGC <u>ATGAGCAACC</u>	AACATTTTCA	AGG <u>TATCATC</u>	CTGATGCGCA
1101	ATATCGGCAT	CGGTTAGCCA	TAACCATTTT	ACCTGTCCGG CGGCCTTAAT
1151	ACCTTGATCA	GATGGTTCGT	GGTGTGTGTA	CCTTGCCGAA GGGCACCGGT
1201	AAAAATGTTC	GCGTCGGTGT	TTTCGCCCGT	GGCCCGAAAG CTGAAGAAGC
1251	TAAAGCTGCT	GGTGCAGAAG	TTGTCGGCGC	AGAAGACCTG ATGGAAGCCA

1301 TTCAGGGCGG CAGCATTGAT TTCGATCGTG ATGCCCTTTA TACTGAAATT

1351 GCCTTGCGCT GCCATAATGA AGCAGCCTCC GGTGTTTTGG CAGATTTAAG

Shine-Dalgarno
1401 CGCTGCCTGA TTTTCGTgat cctctagagt ctatgaaatg gagattcatt

celZ coding region-->
1451 tatgccctctc tcttattcgg ataaccatcc agtcatccgc aagcttggcc

[illegible]

Fig. 6

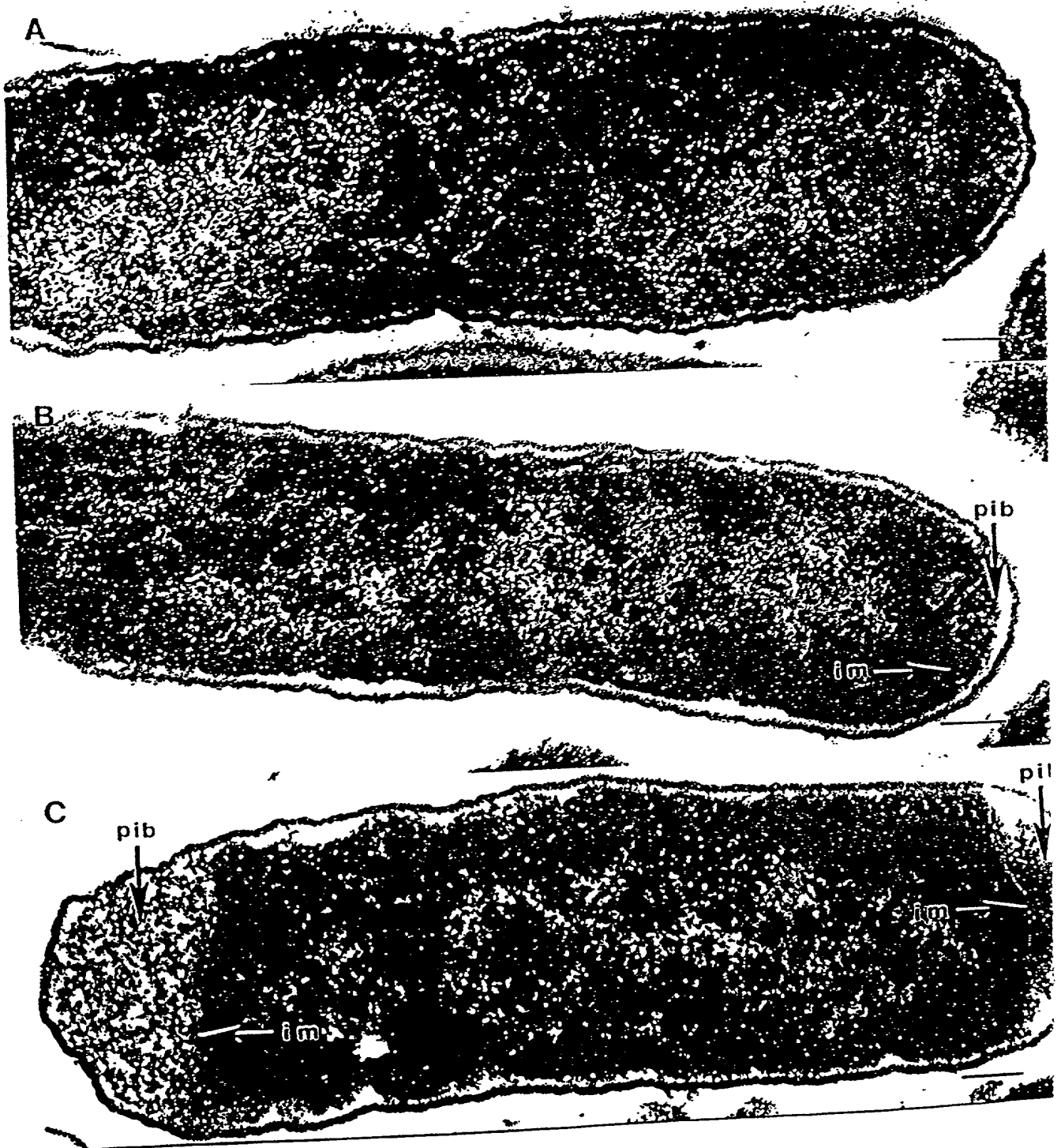


Fig. 7

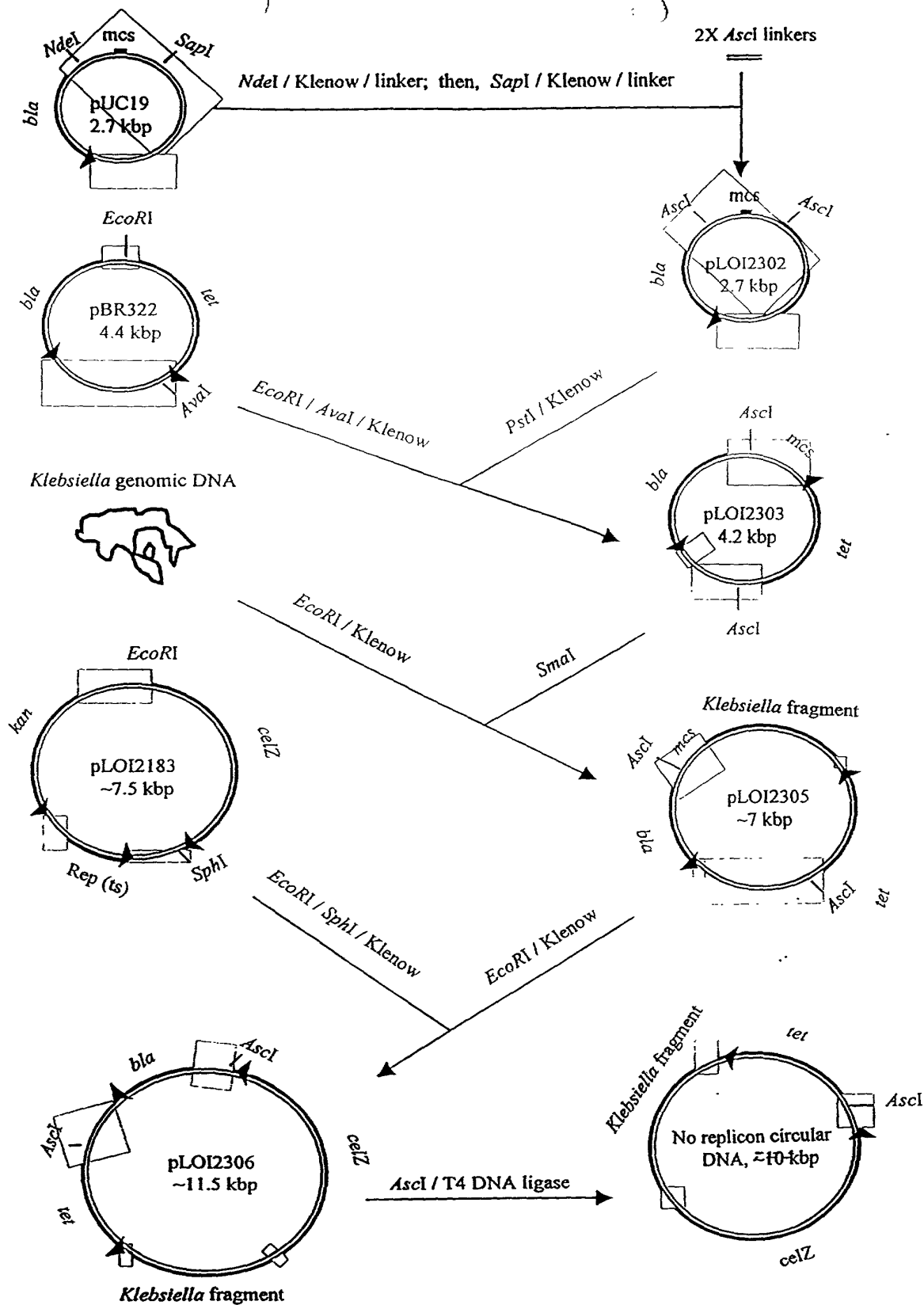
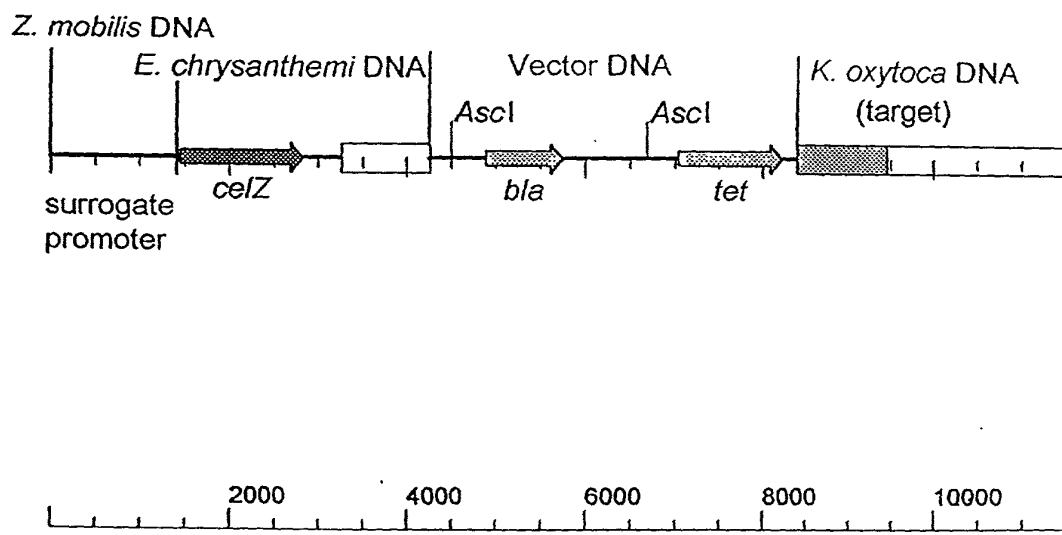


Fig. 8



pLOI2306 (11520 bps)

Fig. 9

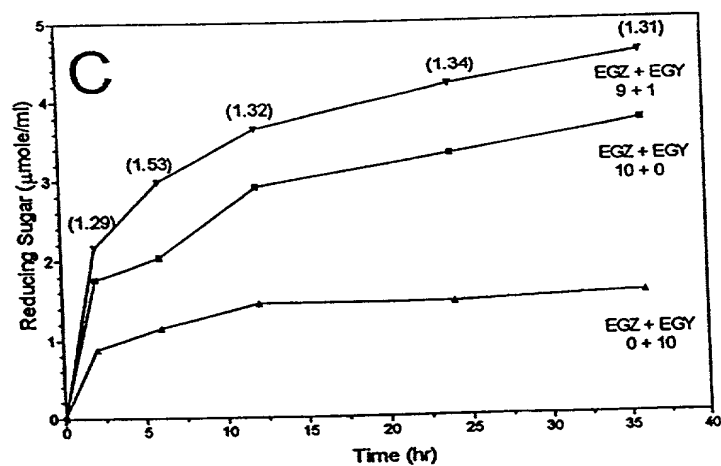
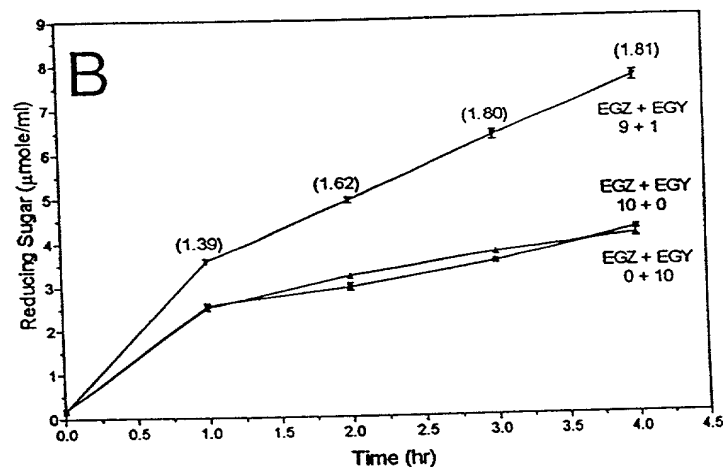
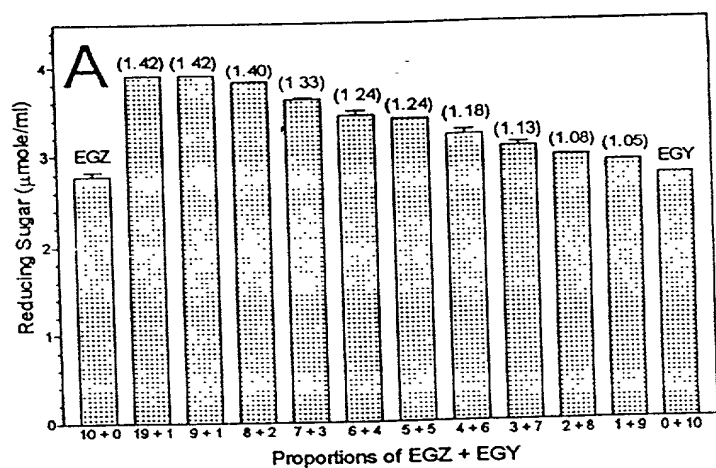
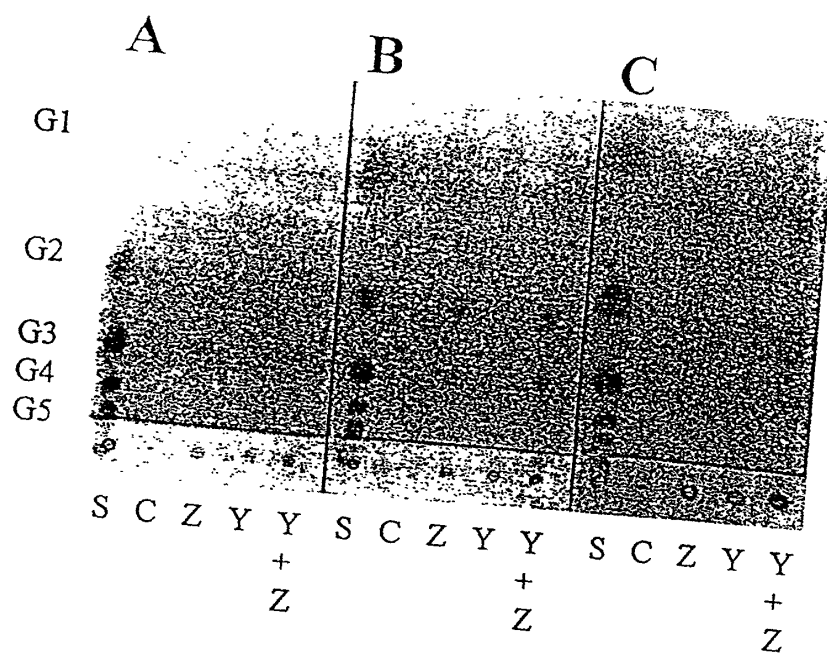


Fig. 10



6465237 061901

Fig. 11

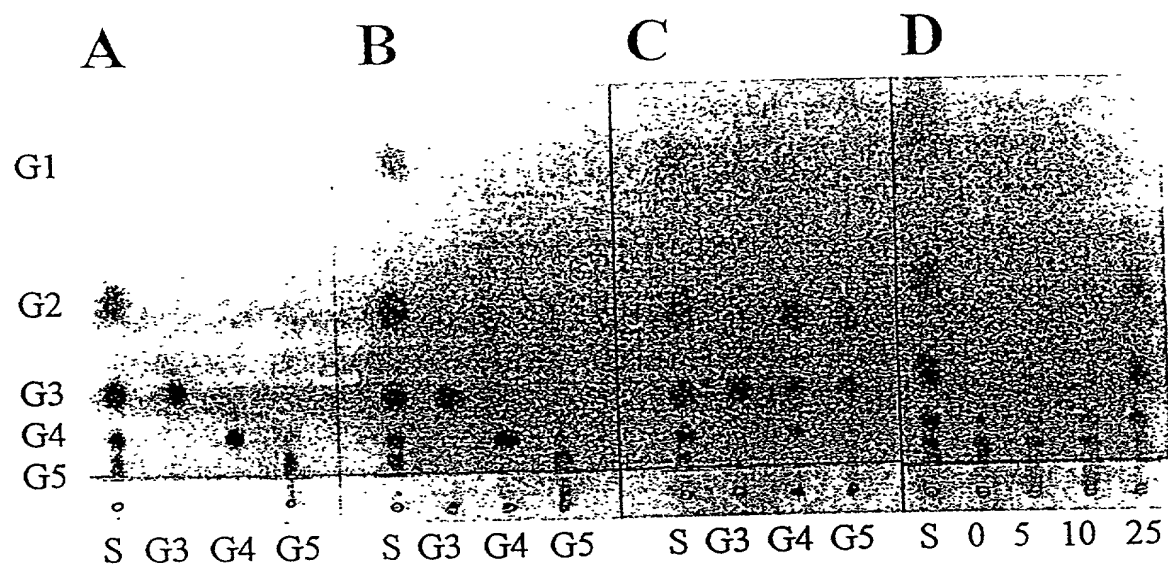


Fig. 12

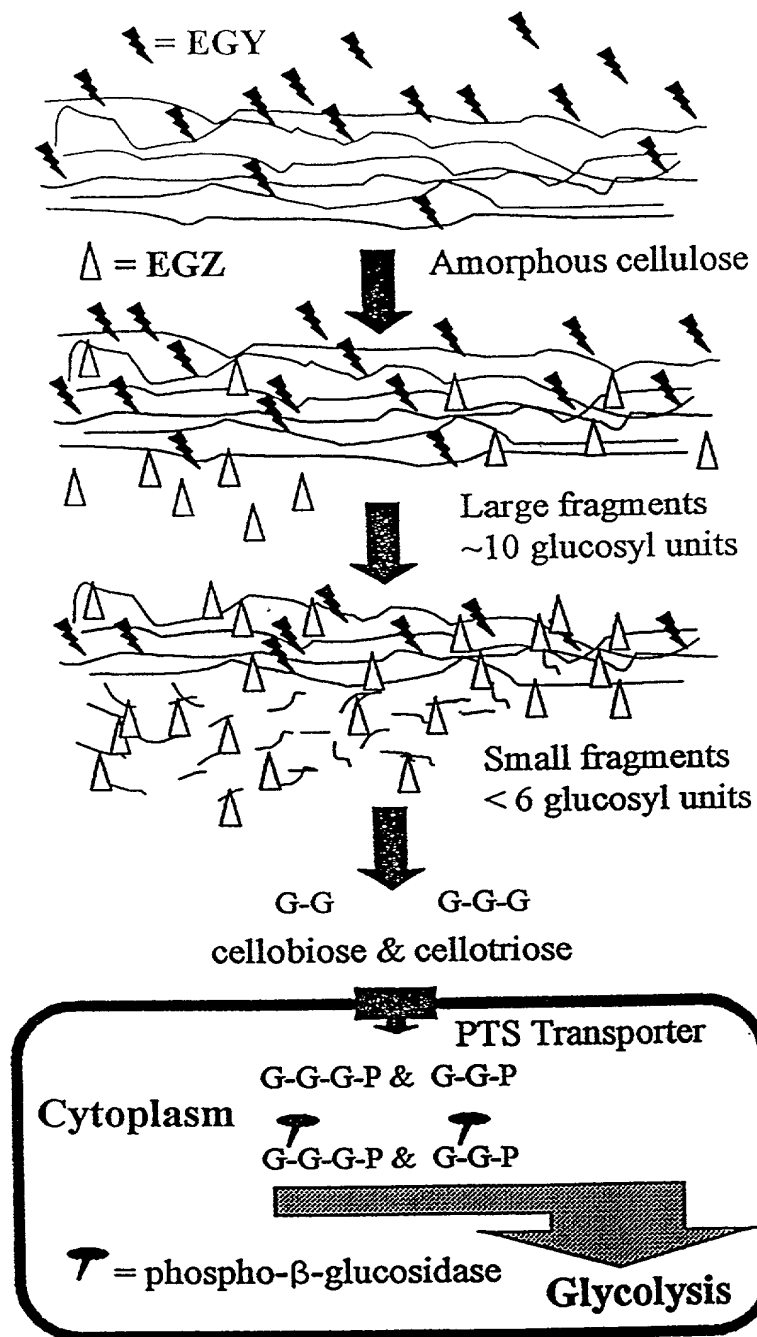


Fig. 13

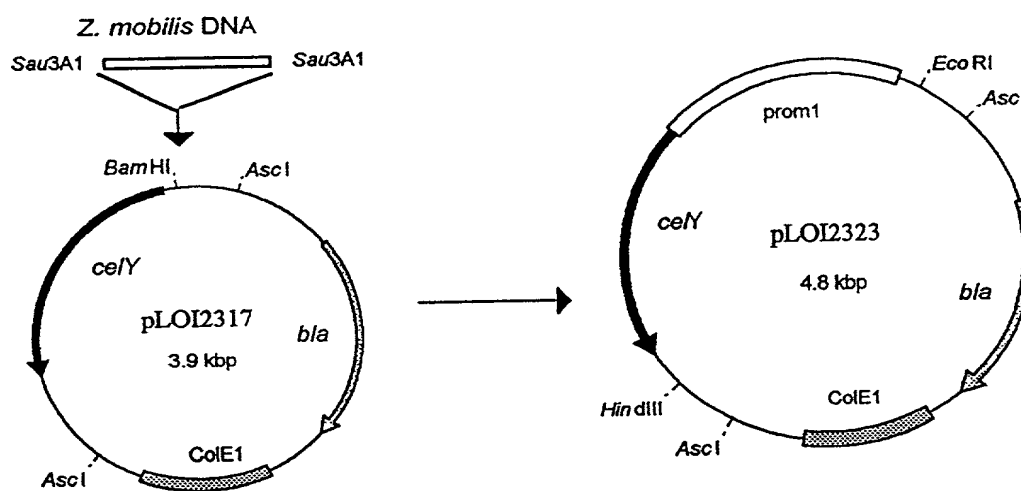
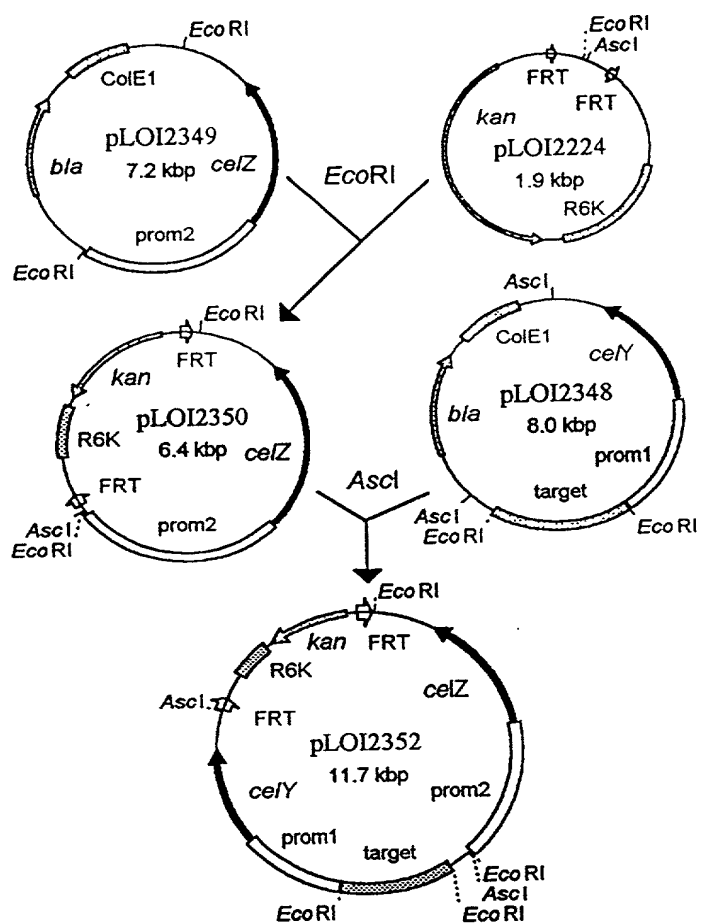


Fig. 14

Position (bp)	-35	-10	RNA Start	Proposed δ factors	δ factor consensus sequence	
					-35	-10
	ATATTTTIGATTTTCAAGAAAGCCTGATATCTTCCAACATCTT		T (2)	δ^{70}	TTGACA	TATAAT
	GATTTGATCCTCTAGAGTCAACCTGCTTGTACTCGTGATCCCAT		A (4)	δ^{70}	TTGACA	TATAAT
	GAGTCAACCTGCTTGTACTCGTGATCCCATTCACAAGGGCGAA		C (1)	δ^{32}	CTTGAA	CCCCAT
	TTACTCGTGATCCCATTCACAAGGGCGAAATTAATTCGCCCTT		C (3)	δ^{38}	CCGCCT	TATACT

* Transcriptional starts for *celY* were identified by primer extension analysis. Four promoters were identified. Upstream sequence of these promoters with similarity to *E. coli* -35 and -10 regions are marked with underlines. RNA start sites are bolded. Putative promoters are numbered in parenthesis adjacent to the start site in descending order from the strongest. Differences in intensities were small, within 2-fold.

Fig. 15



106T00/26233660

Fig. 16

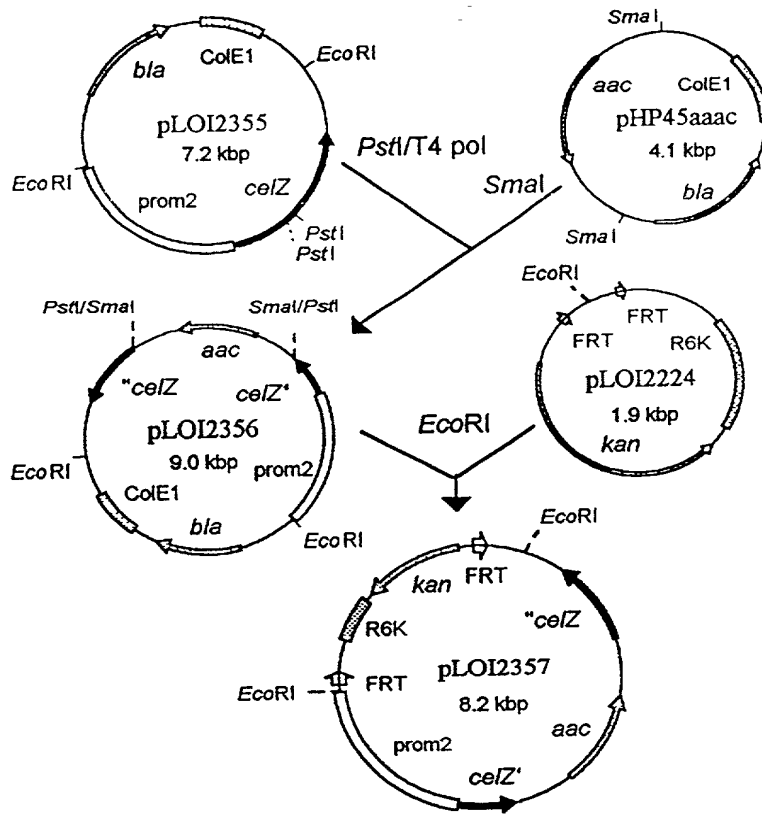


Fig. 17

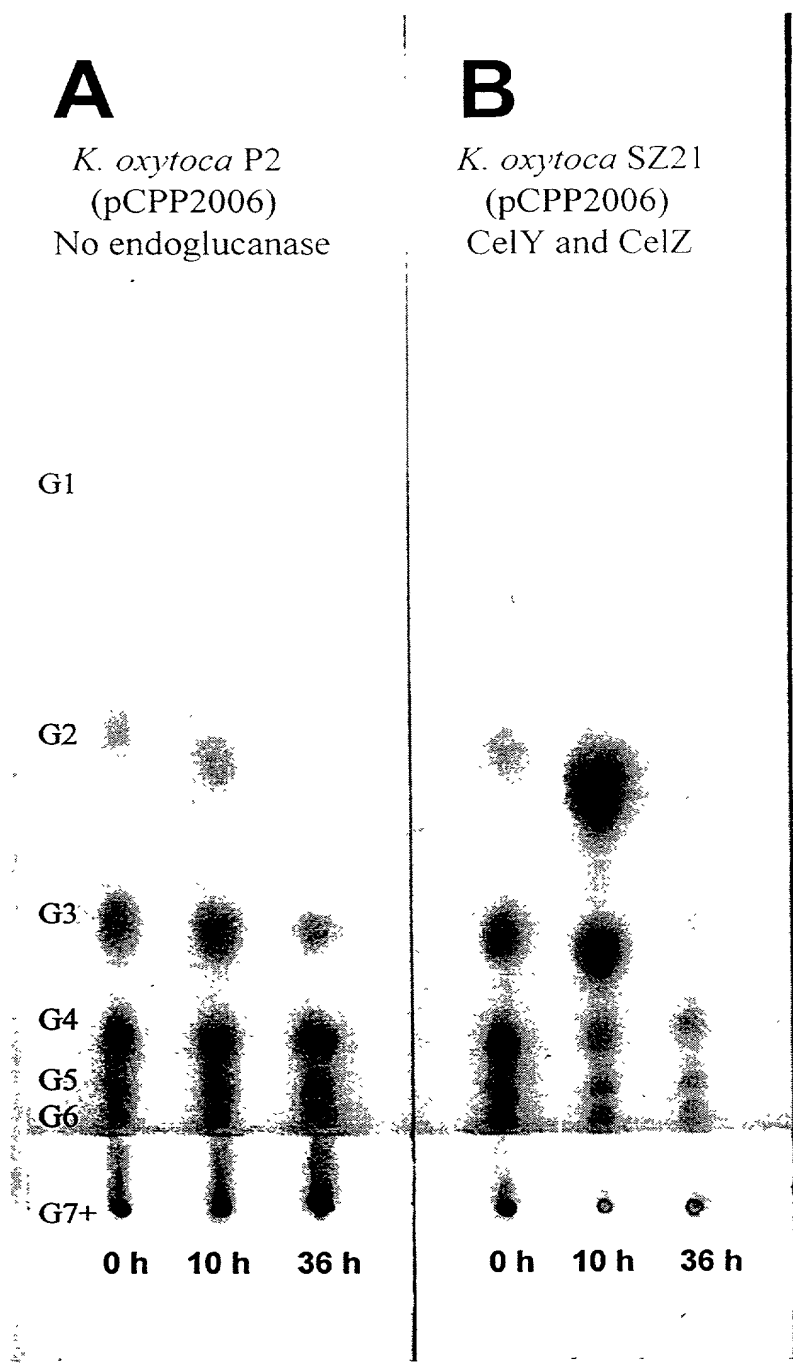


Fig. 18

